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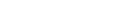


FIG.1

GCCAGGCACCATGGTGCAGAAGTCGCGCAACGGCGGCGTATAGCCCCGGCCCGAG CGGGGAGAAGAAGCTGAAGGTGGGCTTCGTGGGGCTGGACCCCGGCGCCCCGA CTCCACCGGGACGGGCGCTGCTGATCGCCGGCTCCGAGGCCCCCAAGCGCGG GCGCAACGCCTTCTACCGCAAGCTGCAGAATTTCCTCTACAACGTGCTGGAGCGG CCGCGCGCTGGCGTTCATCTACCACGCCTACGTGTTCCTCCTGGTTTTCTCCTG 10 CCTCGTGCTGTCTGTTTTCCACCATCAAGGAGTATGAGAAGAGCTCGGAGGGG GCCCTCTACATCCTGGAAATCGTGACTATCGTGGTGTTTTGGCGTGGAGTACTTCG TGCGGATCTGGGCCGCAGGCTGCTGCTGCCGGTACCGTGGCTGGAGGGGGCGGC TCAAGTTTGCCCGGAAACCGTTCTGTGTGATTGACATCATGGTGCTCATCGCCTC CATTGCGGTGCTGCCGCCGGCTCCCAGGGCAACGTCTTTGCCACATCTGCGCTC CGGAGCCTGCGCTTCCTGCAGATTCTGCGGATGATCCGCATGGACCGGCGGGGA GGCACCTGGAAGCTGCTGGGCTCTGTGGTCTATGCCCACAGCAAGGAGCTGGTC ACTGCCTGGTACATCGGCTTCCTTTGTCTCATCCTGGCCTCGTTCCTGGTGTACTT GGCAGAGAGGGGGAGAACGACCACTTTGACACCTACGCGGATGCACTCTGGTG GGGCCTGATCACGCTGACACCATTGGCTACGGGGACAAGTACCCCCAGACCTGG AACGCAGGCTCCTTGCGGCAACCTTCACCCTCATCGGTGTCTCCTTCTTCGCGCT GCCTGCAGGCATCTTGGGGTCTGGGTTTGCCCTGAAGGTTCAGGAGCAGCACAG GCAGAAGCACTTTGAGAAGAGGCGGAACCCGGCAGCAGGCCTGATCCAGTCGGC CTGGAGATTCTACGCCACCAACCTCTCGCGCACAGACCTGCACTCCACGTGGCAG TACTACGAGCGAACGGTCACCGTGCCCATGTACAGTTCGCAAACTCAAACCTACG GGGCCTCCAGACTTATCCCCCCGCTGAACCAGCTGGAGCTGCTGAGGAACCTCAA GAGTAAATCTGGACTCGCTTTCAGGAAGGACCCCCCGCCGGAGCCGTCTCCAAG CCAGAAGGTCAGTTTGAAAGATCGTGTCTTCTCCAGCCCCGAGGCGTGGCTGCC AAGGGGAAGGGTCCCCGCAGGCCCAGACTGTGAGGCGGTCACCCAGCGCCGAC CAGAGCCTCGAGGACAGCCCCAGCAAGGTGCCCAAGAGCTGGAGCTTCGGGGAC CGCAGCCGGGCACGCCAGGCTTTCCGCATCAAGGGTGCCGCGTCACGGCAGAAC TCAGAAGAAGCAAGCCTCCCGGAGAGGACATTGTGGATGACAAGAGCTGCCCC

TGCGAGTTTGTGACCGAGGACCTGACCCCGGGCCTCAAAGTCAGCATCAGAGCC GTGTGTGTCATGCGGTTCCTGGTGTCCAAGCGGAAGTTCAAGGAGAGCCTGCGGC CCTACGACGTGATGGACGTCATCGAGCAGTACTCAGCCGGCCACCTGGACATGCT GTCCCGAATTAAGAGCCTGCAGTCCAGAGTGGACCAGATCGTGGGGCGGGGCCC AGCGATCACGGACAAGGACCGCACCAAGGGCCCGGCCGAGGCGGAGCTGCCCG 5 AGGACCCCAGCATGATGGGACGGCTCGGGAAGGTGGAGAAGCAGGTCTTGTCCA TGGAGAAGAAGCTGGACTTCCTGGTGAATATCTACATGCAGCGGATGGGCATCC CCCCGACAGAGCCGAGGCCTACTTTGGGGCCAAAGAGCCGGAGCCGGCGCCGC CGTACCACAGCCGGAAGACAGCCGGGAGCATGTCGACAGGCACGGCTGCATTG TCAAGATCGTGCGCTCCAGCAGCTCCACGGGCCAGAAGAACTTCTCGGCGCCCC 10 CGGCCGCCCCTGTCCAGTGTCCGCCCTCCACCTCCTGGCAGCCACAGAGCCA CCCGCGCCAGGGCCACGCACCTCCCCGTGGGGGACCACGGCTCCCTGGTGCG . CATCCCGCCGCCGCCTGCCCACGAGCGGTCGCTGTCCGCCTACGGCGGGGGCAA CCGCGCCAGCATGGAGTTCCTGCGGCAGGAGGACACCCCGGGCTGCAGGCCCCC 15 CGAGGAGCTGGAGCGTTCCTTCAGCGCTTCAGCATCTCCCAGTCCAAGGAGAA CCTGGATGCTCTCAACAGCTGCTACGCGGCCGTGGCGCCTTGTGCCAAAGTCAGG CCCTACATTGCGGAGGGAGAGTCAGACACCGACTCCGACCTCTGTACCCCGTGCG GGCCCCGCCACGCTCGGCCACCGGCGAGGGTCCCTTTGGTGACGTGGGCTGGG 20 CCGGGCCCAGGAAGTGAGGCGGCGCTGGGCCAGTGGACCCGCCGCGGCCCTCC TCAGCACGGTGCCTCCGAGGTTTTGAGGCGGGAACCCTCTGGGGCCCTTTTCTTA CAGTAACTGAGTGTGGCGGGAAGGGTGGGCCCTGGAGGGCCCATGTGGGCTGA AGGATGGGGGCTCCTGGCAGTGACCTTTTACAAAAGTTATTTTCCAACAGGGGCT GGAGGCTGGGCAGGGCCCTGTGCTCCAGGAGCAGCGTGCAGGAGCAAGGCTG 25 CCCTGTCCACTCTGCTCAGGGCCGCCGGCCGACATCAGCCCGGTGTGAGGAGGGG CGGGAGTGATGACGGGGTGTTGCCAGCGTGGCAACAGGCGGGGGTTGTCTCAG CCGAGCCCAGGGGAGGCACAAAGGGCAGGCCTGTTCCCTGAGGACCTGCGCAAA

GGGCGGCCTGTTTGGTGAGGACCTGCGGCCTTGGGTC

ATGGTGCAGAAGTCGCGCAACGGCGGCGTATACCCCGGCCCGAGCGGGGAGAAG AAGCTGAAGGTGGGCTTCGTGGGGCTGGACCCCGGCGCCCGACTCCACCCGG GACGGGGCGCTGCTGATCGCCGGCTCCGAGGCCCCCAAGCGCGCAGCATCCTC AGCAAACCTCGCGCGGGCGCGCGGGCGCCGGGAAGCCCCCAAGCGCAACGC CTTCTACCGCAAGCTGCAGAATTTCCTCTACAACGTGCTGGAGCGGCCGCGCGC 10 TGGGCGTTCATCTACCACGCCTACGTGTTCCTCCTGGTTTTCTCCTGCCTCGTGCT GTCTGTGTTTTCCACCATCAAGGAGTATGAGAAGAGCTCGGAGGGGCCCTCTAC ATCCTGGAAATCGTGACTATCGTGGTGTTTTGGCGTGGAGTACTTCGTGCGGATCT GGGCCGCAGGCTGCTGCCGGTACCGTGGCTGGAGGGGGCGCTCAAGTTTG CCCGGAAACCGTTCTGTGTGATTGACATCATGGTGCTCATCGCCTCCATTGCGGT GCTGGCCGCCGGCTCCCAGGGCAACGTCTTTGCCACATCTGCGCTCCGGAGCCTG 15 CGCTTCCTGCAGATTCTGCGGATGATCCGCATGGACCGGCGGGGAGGCACCTGG AAGCTGCTGGGCTCTGTGGTCTATGCCCACAGCAAGGAGCTGGTCACTGCCTGGT ACATCGGCTTCCTTGTCTCATCCTGGCCTCGTTCCTGGTGTACTTGGCAGAGAAG GGGGAGACGACCACTTTGACACCTACGCGGATGCACTCTGGTGGGGCCTGATC 20 ACGCTGACCACCATTGGCTACGGGGACAAGTACCCCCAGACCTGGAACGGCAGG CATCTTGGGGTCTGGGTTTGCCCTGAAGGTTCAGGAGCAGCACAGGCAGAAGCA CTTTGAGAAGAGGCGGAACCCGGCAGCAGGCCTGATCCAGTCGGCCTGGAGATT CTACGCCACCAACCTCTCGCGCACAGACCTGCACTCCACGTGGCAGTACTACGAG 25 CGAACGGTCACCGTGCCCATGTACAGTTCGCAAACTCAAACCTACGGGGCCTCCA GACTTATCCCCCCGCTGAACCAGCTGGAGCTGCTGAGGAACCTCAAGAGTAAAT CTGGACTCGCTTTCAGGAAGGACCCCCGCCGGAGCCGTCTCCAAGCCAGAAGG TCAGTTTGAAAGATCGTGTCTTCTCCAGCCCCCGAGGCGTGGCTGCCAAGGGGAA GGGGTCCCGCAGGCCCAGACTGTGAGGCGGTCACCCAGCGCCGACCAGAGCCT 30 CGAGGACAGCCCAGCAAGGTGCCCAAGAGCTGGAGCTTCGGGGACCGCAGCCG GGCACGCCAGGCTTTCCGCATCAAGGGTGCCGCGTCACGGCAGAACTCAGAAGA

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AGCAAGCCTCCCGGAGAGGACATTGTGGATGACAAGAGCTGCCCCTGCGAGTT CATGCGGTTCCTGGTGTCCAAGCGGAAGTTCAAGGAGAGCCTGCGGCCCTACGA CGTGATGGACGTCATCGAGCAGTACTCAGCCGGCCACCTGGACATGCTGTCCCGA ATTAAGAGCCTGCAGTCCAGAGTGGACCAGATCGTGGGGCCGGGGCCCAGCGATC ACGGACAAGGACCGCACCAAGGGCCCGGCCGAGGCGGAGCTGCCCGAGGACCC CAGCATGATGGGACGCTCGGGAAGGTGGAGAAGCAGGTCTTGTCCATGGAGAA GAAGCTGGACTTCCTGGTGAATATCTACATGCAGCGGATGGGCATCCCCCGACA GAGACCGAGGCCTACTTTGGGGCCAAAGAGCCGGAGCCGGCGCCGCCGTACCAC AGCCCGGAAGACAGCCGGGAGCATGTCGACAGGCACGGCTGCATTGTCAAGATC GTGCGCTCCAGCAGCTCCACGGGCCAGAAGAACTTCTCGGCGCCCCCGGCCGCG CCCCTGTCCAGTGTCCGCCCTCCACCTCCTGGCAGCCACAGAGCCACCCGCGCC AGGGCCACGGCACCTCCCCGTGGGGGACCACGGCTCCCTGGTGCGCATCCCGC CGCCGCCTGCCCACGAGCGGTCGCTGTCCGCCTACGGCGGGGGCAACCGCGCCA GCATGGAGTTCCTGCGGCAGGAGGACACCCCGGGCTGCAGGCCCCCCGAGGGGA TGGAGCGTTCCTTCAGCGGCTTCAGCATCTCCCAGTCCAAGGAGAACCTGGATGC TCTCAACAGCTGCTACGCGGCCGTGGCGCCTTGTGCCAAAGTCAGGCCCTACATT GCGGAGGGAGAGTCAGACACCGACTCCGACCTCTGTACCCCGTGCGGGCCCCCG CCACGCTCGGCCACCGGCGAGGGTCCCTTTGGTGACGTGGGCTGGGCCGGGCCC **AGGAAGTGA**

Human Brain-Derived Potassium Channel DNA Structural Region · SEQ ID NO:2

MVQKSRNGGVYPGPSGEKKLKVGFVGLDPGAPDSTRDGALLIAGSEAPKRGSILSKP RAGGAGAGKPPKRNAFYRKLQNFLYNVLERPRGWAFIYHAYVFLLVFSCLVLSVFS TIKEYEKSSEGALYILEIVTIVVFGVEYFVRIWAAGCCCRYRGWRGRLKFARKPFCVI DIMVLIASIAVLAAGSQGNVFATSALRSLRFLQILRMIRMDRRGGTWKLLGSVVYAH SKELVTAWYIGFLCLILASFLVYLAEKGENDHFDTYADALWWGLITLTTIGYGDKYP QTWNGRLLAATFTLIGVSFFALPAGILGSGFALKVQEQHRQKHFEKRRNPAAGLIQS AWRFYATNLSRTDLHSTWQYYERTVTVPMYSSQTQTYGASRLIPPLNQLELLRNLKS 10 KSGLAFRKDPPPEPSPSQKVSLKDRVFSSPRGVAAKGKGSPQAQTVRRSPSADQSLE DSPSKVPKSWSFGDRSRARQAFRIKGAASRQNSEEASLPGEDIVDDKSCPCEFVTEDL TPGLKVSIRAVCVMRFLVSKRKFKESLRPYDVMDVIEQYSAGHLDMLSRIKSLQSRV DQIVGRGPAITDKDRTKGPAEAELPEDPSMMGRLGKVEKQVLSMEKKLDFLVNIYM QRMGIPPTETEAYFGAKEPEPAPPYHSPEDSREHVDRHGCIVKIVRSSSSTGQKNFSAP 15 PAAPPVQCPPSTSWQPQSHPRQGHGTSPVGDHGSLVRIPPPPAHERSLSAYGGGNRAS MEFLRQEDTPGCRPPEGTLRDSDTSISIPSVDHEELERSFSGFSISQSKENLDALNSCYA AVAPCAKVRPYIAEGESDTDSDLCTPCGPPPRSATGEGPFGDVGWAGPRK*

20 Human Brain-Derived Potassium Channel Peptide [Residue Sequence] · SEQ ID NO:3

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FIG.4

GCGGAACCGCCCCCCGGCCATGCGGCTCCCGGCCGGGGGGCCTGGGCTGGGC CCGCGCCCCCCGCGCTCCGCCCCCGCTGAGCCCGACCCGGGGCCC CTCCCGCCAGGCACCATGGTGCAGAAGTCGCGCAACGGCGGCGTATACCCCGGC CCGAGCGGGGAGAAGAAGCTGAAGGTGGGCTTCGTGGGGCTGGACCCCGGCGCG CCCGACTCCACCGGGACGGGGCGCTGCTGATCGCCGGCTCCGAGGCCCCCAAG CGCGGCAGCATCCTCAGCAAACCTCGCGCGGGCGCGGGGGGCGCCGGGAAGCCC CCCAAGCGCAACGCCTTCTACCGCAAGCTGCAGAATTTCCTCTACAACGTGCTGG AGCGGCCGCGCGCTGGGCGTTCATCTACCACGCCTACGTGTTCCTCCTGGTTTT CTCCTGCCTCGTGCTGTCTTTTCCACCATCAAGGAGTATGAGAAGAGCTCG GAGGGGCCCTCTACATCCTGGAAATCGTGACTATCGTGGTGTTTTGGCGTGGAGT ACTTCGTGCGGATCTGGGCCGCAGGCTGCTGCTGCCGGTACCGTGGCTGGAGGG GGCGGCTCAAGTTTGCCCGGAAACCGTTCTGTGTGATTGACATCATGGTGCTCAT CGCCTCCATTGCGGTGCTGGCCGCCGGCTCCCAGGGCAACGTCTTTGCCACATCT GCGCTCCGGAGCCTGCGCTTCCTGCAGATTCTGCGGATGATCCGCATGGACCGGC GGGGAGCACCTGGAAGCTGCTGGGCTCTGTGGTCTATGCCCACAGCAAGGAGC TGGTCACTGCCTGGTACATCGGCTTCCTTTGTCTCATCCTGGCCTCGTTCCTGGTG TACTTGGCAGAGAGGGGGAGAACGACCACTTTGACACCTACGCGGATGCACTC TGGTGGGCCTGATCACGCTGACCACCATTGGCTACGGGGACAAGTACCCCCAG ACCTGGAACGCAGGCTCCTTGCGGCAACCTTCACCCTCATCGGTGTCTCCTTCT TCGCGCTGCCTGCAGGCATCTTGGGGTCTGGGTTTGCCCTGAAGGTTCAGGAGCA GCACAGGCAGAAGCACTTTGAGAAGAGGCGGAACCCGGCAGCAGGCCTGATCCA GTCGGCCTGGAGATTCTACGCCACCAACCTCTCGCGCACAGACCTGCACTCCACG TGGCAGTACTACGAGCGAACGGTCACCGTGCCCATGTACAGGTACCGCCGCCGG GCACCTGCCACCAAGCAACTGTTTCATTTTTTTTTTTCCATTTGTTCT**TAA**ACCCC

30 AAGG

Yokoyama et al cDNA Sequence (HNSPC) (Genbank accession # D82346)

SEQ ID NO:4

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FIG.5

MVQKSRNGGVYPGPSGEKKLKVGFVGLDPGAPDSTRDGALLIAGSEAPKRGSILSKP RAGGAGAGKPPKRNAFYRKLQNFLYNVLERPRGWAFIYHAYVFLLVFSCLVLSVFS TIKEYEKSSEGALYILEIVTIVVFGVEYFVRIWAAGCCCRYRGWRGRLKFARKPFCVI DIMVLIASIAVLAAGSQGNVFATSALRSLRFLQILRMIRMDRRGGTWKLLGSVVYAH SKELVTAWYIGFLCLILASFLVYLAEKGENDHFDTYADALWWGLITLTTIGYGDKYP QTWNGRLLAATFTLIGVSFFALPAGILGSGFALKVQEQHRQKHFEKRRNPAAGLIQS AWRFYATNLSRTDLHSTWQYYERTVTVPMYRYRRRAPATKQLFHFLFSICS* 10

Yokoyama et al amino acid sequence (HNSPC) · SEQ ID NO:5

FIG.6

METRGSRLTGGQGRVYNFLERPTGWKCFVYHFAVFLIVLVCLIFSVLSTIEQYAALAT
GTLFWMEIVLVVFFGTEYVVRLWSAGCRSKYVGLWGRLRFARKPISIIDLIVVVASM
VVLCVGSKGQVFATSAIRGIRFLQILRMLHVDRQGGTWRLLGSVVFIHRQELITTLYI
GFLGLIFSSYFVYLAEKDAVNESGRVEFGSYADALWWGVVTVTTIGYGDKVPQTWV
GKTIASCFSVFAISFFALPAGILGSGFALKVQQKQRQKHFNRQIPAAASLIQTAWRCY
AAENPDSSTWKIYIRKAPRSHTLLSPSPKPKKSVVVKKKKFKLDKDNGVTPGEKMLT
VPHITCDPPEERRLDHFSVDGYDSSVRKSPTLLEVSMPHFMRTNSFAEDLDLEGETLL
TPITHISQLREHHRATIKVIRRMQYFVAKKKFQQARKPYDVRDVIEQYSQGHLNLMV
RIKELQRRLDQSIGKPSLFISVSEKSKDRGSNTIGARLNRVEDKVTQLDQRLALITDML
HQLLSLHGGSTPGSGGPPREGGAHITQPCGSGGSVDPELFLPSNTLPTYEQLTVPRRG
PDEGS

Sanguinetti et al amino acid sequence (HKvLQT1) (Genbank Accession U40990, U71077)

SEQ ID NO:6

FIG.7

| ,, | 24, 1997 10:45 AM | | | | |
|---------------|--------------------|-----------------|---------------------|--|------------------|
| | 10 | 20 | 30 | 40 | 50 |
| | | | | RDGALLIAGSE | |
| | NGGVYPGPS | GERRLRUGPV | GLDPGAPDST | RDGALLIAGSE | - E TR SEQ ID NO |
| | 60 | 70 | 80 | 90 | 100 |
| | | | | ERPRGWAFIYH | |
| GSILSK | PRAGGAGAG | KPPKRHAFYR | KLONPLYNVL | ERPRGWAFIYH ERPTGWCPVYH | AYVF SEQ ID MO |
| <u> </u> | GGIQI <u>G</u> | 18 | VI MFL | TKN: G #CEPVER | |
| | 110 | 120 | 130 | 140 | 150 |
| LLVFSCI | VLSVESTI | KRYEKSSEGA | LVILRIVTIV | VFGVEYPVRIW VFG <u>V</u> EY <u>P</u> VRIW | AAGC SEO ID NO |
| LIVL VC | IFS VLS TI | EQYAALATGT | LFWMEIVLVV | PPGTE YVV RLW | SAGC SEQ ID NO |
| | 160 | 170 | 180 | 190 | 200 |
| | | | | GSQGNVPATSA | |
| | | | | G S Q G N V F A T S A G S K G Q V F A T S A | |
| | | | | 00,000,000 | |
| | 210 | 220 | 230 | 240 | 250 |
| | | | | WYIGFLCLILA WYIGFLCLILA | |
| | | | | LYIGPLGLIFS | |
| | 260 | 270 | 280 | 290 | 300 |
| | | | | GDKYPQTWNGR | |
| | | | | GDKYPQTWNGR GDKVPQTWVGK | |
| | | <u> </u> | | | |
| | 310 | 320 | 330 | 340 | 350 |
| | | | | KRRNPAAGLIQ KRRNPAAGLIQ | |
| | | | | RQIPAAASLIQ | |
| | 360 | 370 | 380 | 390 | 400 |
| | | | | ASRLIPPLNQL | ELLR SEQ ID NO |
| | | QYYERTVTVP | | LL SPSPRP | SEQ ID NO |
| - IN A B OF E | DS <u>[S 1 M</u>] | KIJIKKAP | <u>RS</u> HEJ | FILSESPAP | KKS V SEQ ID A |
| | 410 | 420 | 430 | 440 | 450 |
| n r K s K s c | | PEPSPSQKVS | L K D R V F S S P R | GVAAKGKGSPQ | A Q SEQ ID NO |
| | | N C V TPG EKM L | TVPHITCDPP | EERRLDHFSVD | |
| | 460 | 470 | 480 | 490 | 500 |
| TVRRSPS | | | | RIKGAASRQNS | |
| | | | | | SEQ ID NO |

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FIG.7 (p.2)

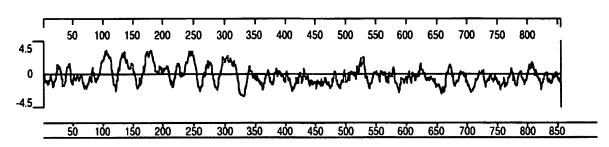
| nment Report of Fit iday, November 24, | | Justal method with PAM250 | 0 residue weight table | 2. | Page |
|---|---------------|---------------------------|-------------------------|---|---------------------------|
| LELY, NOVELLEGI EX | 510 | 520 | 530 | 540 | 550 |
| LPGEDIV | DDKSCPC | EFYTEDLTPGL | | VMRP L VSKRK PK | |
| <u> </u> | | | | LPHPL | OARKP SEO ID NO |
| LEGET L L | T [P] I | тні зо-цванн | RATEIRVIR | HEO Y POAKE E PO | OWKKE SEO ID PO |
| | 560 | 570 | 580 | 590 | 600 |
| YDVMDVI | BQYSAGH | LDMLSRIKSLO | SRVDQIVG | RGPAITDKD | RTKGP SEQ ID NO |
| | | | م تحادما | K P S L F I S V S E K S | SEQ ID NO |
| YDVRDVI | ROYSIQIGH | EN L M VIR I KIBIL Q | lakir <u>n ö</u> ls i G | KPSLFISVSEEDS | K D K G S SEQ 1D NO |
| | 610 | 620 | 630 | 640 | 650 |
| AEAELPE: | D P S M M G R | LGKVEKQVLSM | EKKLDFLV | NIYMQRMGIPPT | ETEAY SEQ ID NO |
| | | LIN RV ED KVT Q L | 2000 | 2 | SEQ ID NO |
| | FIGA <u>K</u> | Da KA PA KALA F | DOKENTI | онвидревен | |
| | 660 | 670 | 680 | 690 | 700 |
| PGAKEPE | PAPPYHS | PEDSREHVDRH | GCIVKIVR | SSSSTGQKNFSA | PPAAP SEQ ID NO |
| -GGSTPG | e c c l l | | | | SEQ ID NO |
| - @ G S 1 E G : | 3 G G[P] | | | | |
| | 710 | 720 | 730 | 740 | 750 |
| PVQCPPS | TSWQPQS | H <u>PR</u> QGHGTSPV | G D H G S L V R | IP PPP A H E R S L S | |
| | | -PREG | GAH | IT QPC G | SEQ ID NO |
| | | -(FA) = (U) | (A) W (E) [| III OECO | 3(<u>0 0</u>) 350 10 NO |
| | 760 | 770 | 780 | 790 | 800 |
| NRASMEPI | LRQEDTP | GCRPPEGTLRD | SDTSISIP | SVDHEELERSFS | |
| SVDPELFI | n | PSNTLP- | | | - FSI - SEQ ID NO |
| | 9 | PSWEEP- | | | - |
| | 810 | 820 | 830 | 840 | 850 |
| QSKENLDA | ALNSCYA | AVAPCARVRPY | IAEGESDT | DSDLCTPCGPPP | RISAT G SEQ ID NO |
| | | | | <u> c </u> s. | SEQ ID NO |
| | | | | <u>P</u> | RRGPD SEQ ID NO |
| | 860 | | | | |
| EGPPGDV | SWAGPRK | • | | | SEQ ID NO |
| <u></u> | | | | | SEQ ID NO |
| EGS. | | | | | SEQ ID NO |

Decoration 'Decoration #1': Box residues that match the Consensus exactly

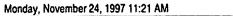
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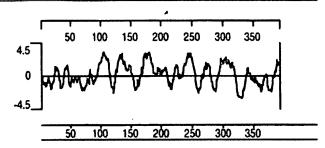
FIG.8

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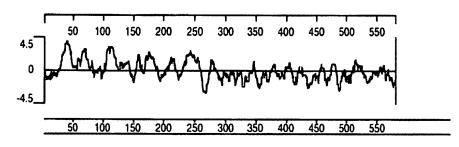
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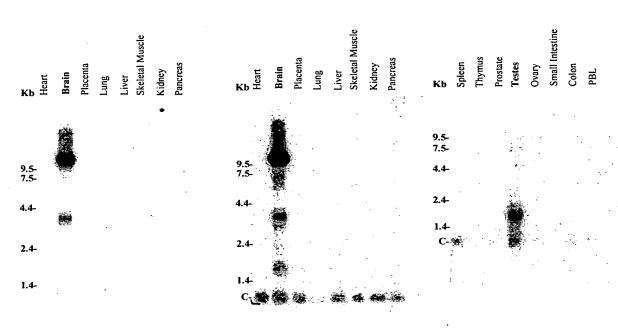


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Monday, November 24, 1997 11:21 AM



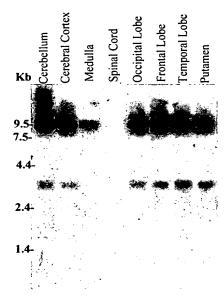
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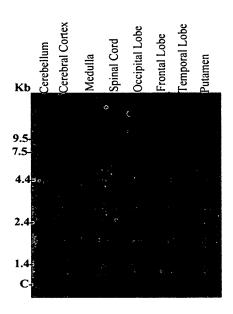
Multiple Tissue Northern I Probe 1 Multiple Tissue Northern I Probe 2 Multiple Tissue Northern II Probe 2

PBL=Peripheral Blood Leukocytes C=700 bp housekeeping cyclophilin transcript, used for normalization of RNA loading

5



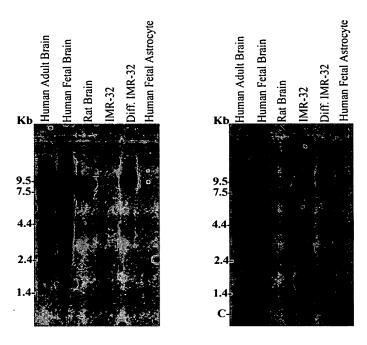
Human Brain Northern Probe 1



Human Brain Northern Probe 2

C=700 bp housekeeping cyclophilin transcript, used for normalization of RNA loading

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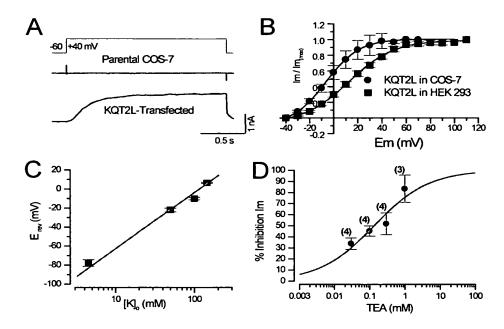


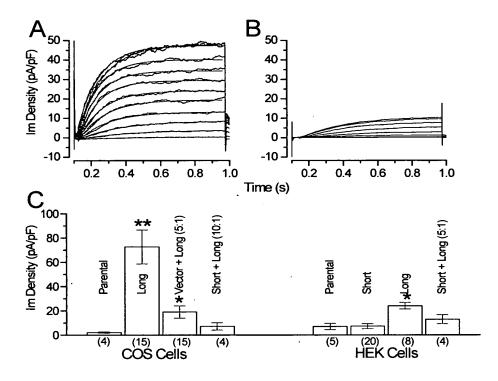
Brain Tissue and Cell Panel Northerns

Probe 1

Probe 2

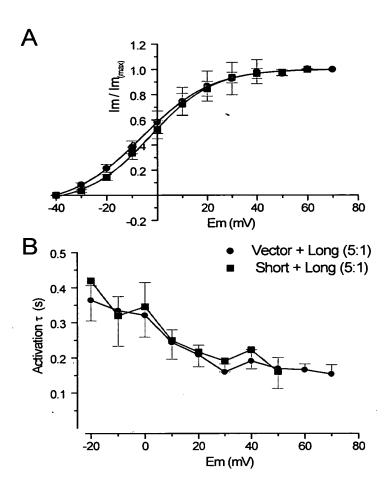
C=700 bp housekeeping cyclophilin transcript, used for normalization of RNA loading

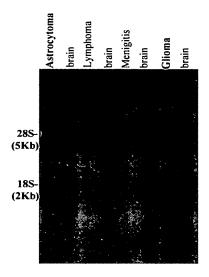




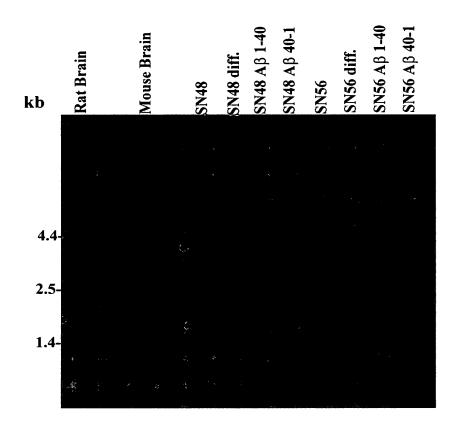














MGLKARRAAGAAGGGGGGGGGGGGAANPAGGDSAVAGDEERKVGLAPGDVEQ VTLALGTGADKDGTLLLEGGGREEGQRRTPQGIGLLAKTPLSRPVKRNNAKYRRIQT LIYDALERPRGWALLYHALVFLIVLGCLILAVLTTFKEYETVSGDWLLVPETFAIFIFG AEFALRIWAAGCCCRYKGWRGRLKFARKPLCMLDIFVLIASVPVVAVGNQGNVLAT SLRSLRFLQILRMLRMDRRGGTWKLLGSAICAHSKELITAWYIGFLTLILSSFLVYLVE KDVPEMDAQGEEMKEEFETYADALWWGLITLATIGYGDKTPKTWEGRLIAATFSLI 10 GVSFFALPAGILGSGLALKVOEOHROKHFEKRRKPAAELIOAAWRYYATNNRLDLV ATWRFYESVVSFPFFRKEQLEAAASQKLGLLDRVRLSNPRGSNTKGKLFTPLNVDAI EESPSKEPKPVGLNNKERFRTAFRMKAYAFWQSSEDAGTGDPMTEDRGYGNDFLIE DMIPTLKAAIRAVRILOFRLYKKKFKETLRPYDVKDVIEOYSAGHLDMLSRIKYLOTR 15 IDMIFTPGPPSTPKHKKSQKGSAFTYPSQQSPRNEPYVARAATSETEDQSMMGKFVK VEROVHDMGKKLDFLVDMHMQHMERLQVHVTEYYPTKGASSPAEGEKKEDNRYS DLKTIICNYSESGPPDPPYSFHOVPIDRVGPYGFFAHDPVKLTRGGPSSTKAQANLPSS GSTYAERPTVLPILTLLDSCVSYHSQTELQGPYSDHISPRQRRSITRDSDTPLSLMSVN HEELERSPSGFSISODRDDYVFGPSGGSSWMREKRYLAEGETDTDTDFFTPSGSMPM SSTGDGISDSIWTPSNKPT 20

SEQ ID NO:7 · Rat KvQT3 (GENBANK Accession Number: AF087454)

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GDVEQVTLALGAGADKDGTLLLEGGGRDEGQRRTPQGIGLLAKTPLSRPVKRNNAK 30 YRRIQTLIYDALERPRGWALLYHALVFLIVLGCLILAVLTTFKEYETVSGDWLLLLET FAIFIFGAEFALRIWAAGCCCRYKGWRGRLKFARKPLCMLDIFVLIASVPVVAVGNQ GNVLATSLRSLRFLQILRMLRMDRRGGTWKLLGSAICAHSKELITAWYIGFLTLILSS FLVYLVEKDVPEVDAQGEEMKEEFETYADALWWGLITLATIGYGDKTPKTWEGRLI AATFSLIGVSFFALPAGILGSGLALKVQEQHRQKHFEKRRKPAAELIQAAWRYYATN PNRIDLVATWRFYESVVSFPFFRKEQLEAASSQKLGLLDRVRLSNPRGSNTKGKLFTP 35 LNVDAIEESPSKEPKPVGLNNKERFRTAFRMKAYAFWQSSEDAGTGDPMAEDRGYG NDFPIEDMIPTLKAAIRAVRILQFRLYKKKFKETLRPYDVKDVIEQYSAGHLDMLSRI KYLQTRIDMIFTPGPPSTPKHKKSQKGSAFTFPSQQSPRNEPYVARPSTSEIEDQSMM GKFVKVERQVQDMGKKLDFLVDMHMQHMERLQVQVTEYYPTKGTSSPAEAEKKE DNRYSDLKTIICNYSETGPPEPPYSFHQVTIDKVSPYGFFAHDPVNLPRGGPSSGKVQ 40 ATPPSSATTYVERPTVLPILTLLDSRVSCHSQADLQGPYSDRISPRQRRSITRDSDTPLS LMSVNHEELERSPSGFSISQDRDDYVFGPNGGSSWMREKRYLAEGETDTDTDPFTPS **GSMPLSSTGDGISDSVWTPSNKPI**